

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: White, Mark Leslie
Carroll, Stephen Fitzhugh
Ma, Jeremy Kam-kuen

(ii) TITLE OF INVENTION: METHOD FOR QUANTIFYING LBP IN BODY FLUIDS

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY INFORMATION:

(A) NAME: Lin-Laures, Li-Hsien
(B) REGISTRATION NUMBER: 33,547
(C) REFERENCE/DOCKET NUMBER: 27129/33783

(ix) TELECOMMUNICATION INFORMATION:

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(C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1443 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1443

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 76..1443

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION: "rLBP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GGG GCC TTG GCC AGA GCC CTG CCG TCC ATA CTG CTG GCA TTG CTG Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu Ala Leu Leu -25 -20 -15 -10	48
CTT ACG TCC ACC CCA GAG GCT CTG GGT GCC AAC CCC GGC TTG GTC GCC Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly Leu Val Ala -5 1 5	96
AGG ATC ACC GAC AAG GGA CTG CAG TAT GCG GCC CAG GAG GGG CTA TTG Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu Gly Leu Leu 10 15 20	144
GCT CTG CAG AGT GAG CTG CTC AGG ATC ACG CTG CCT GAC TTC ACC GGG Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp Phe Thr Gly 25 30 35	192
GAC TTG AGG ATC CCC CAC GTC GGC CGT GGG CGC TAT GAG TTC CAC AGC Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu Phe His Ser 40 45 50 55	240
CTG AAC ATC CAC AGC TGT GAG CTG CTT CAC TCT GCG CTG AGG CCT GTC Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu Arg Pro Val 60 65 70	288
CCT GGC CAG GGC CTG AGT CTC AGC ATC TCC GAC TCC TCC ATC CGG GTC Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser Ile Arg Val 75 80 85	336
CAG GGC AGG TGG AAG GTG CGC AAG TCA TTC AAA CTA CAG GGC TCC Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu Gln Gly Ser 90 95 100	384
TTT GAT GTC AGT GTC AAG GGC ATC AGC ATT TCG GTC AAC CTC CTG TTG Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn Leu Leu Leu 105 110 115	432
GGC AGC GAG TCC TCC GGG AGG CCC ACA GTT ACT GCC TCC AGC TGC AGC Gly Ser Glu Ser Ser Gly Arg Pro Thr Val Thr Ala Ser Ser Cys Ser 120 125 130 135	480
AGT GAC ATC GCT GAC GTG GAG GTG GAC ATG TCG GGA GAC TTG GGG TGG Ser Asp Ile Ala Asp Val Glu Val Asp Met Ser Gly Asp Leu Gly Trp 140 145 150	528
CTG TTG AAC CTC TTC CAC AAC CAG ATT GAG TCC AAG TTC CAG AAA GTA Leu Leu Asn Leu Phe His Asn Gln Ile Glu Ser Lys Phe Gln Lys Val 155 160 165	576
CTG GAG AGC AGG ATT TGC GAA ATG ATC CAG AAA TCG GTG TCC TCC GAT Leu Glu Ser Arg Ile Cys Glu Met Ile Gln Lys Ser Val Ser Ser Asp 170 175 180	624
CTA CAG CCT TAT CTC CAA ACT CTG CCA GTT ACA ACA GAG ATT GAC AGT Leu Gln Pro Tyr Leu Gln Thr Leu Pro Val Thr Glu Ile Asp Ser 185 190 195	672
TTC GCC GAC ATT GAT TAT AGC TTA GTG GAA GCC CCT CGG GCA ACA GCC Phe Ala Asp Ile Asp Tyr Ser Leu Val Glu Ala Pro Arg Ala Thr Ala 200 205 210 215	720
CAG ATG CTG GAG GTG ATG TTT AAG GGT GAA ATC TTT CAT CGT AAC CAC Gln Met Leu Glu Val Met Phe Lys Gly Glu Ile Phe His Arg Asn His 220 225 230	768

CGT TCT CCA GTT ACC CTC CTT GCT GCA GTC ATG AGC CTT CCT GAG GAA Arg Ser Pro Val Thr Leu Leu Ala Ala Val Met Ser Leu Pro Glu Glu 235 240 245	816
CAC AAC AAA ATG GTC TAC TTT GCC ATC TCG GAT TAT GTC TTC AAC ACG His Asn Lys Met Val Tyr Phe Ala Ile Ser Asp Tyr Val Phe Asn Thr 250 255 260	864
GCC AGC CTG GTT TAT CAT GAG GAA GGA TAT CTG AAC TTC TCC ATC ACA Ala Ser Leu Val Tyr His Glu Glu Gly Tyr Leu Asn Phe Ser Ile Thr 265 270 275	912
GAT GAG ATG ATA CCG CCT GAC TCT AAT ATC CGA CTG ACC ACC AAG TCC Asp Glu Met Ile Pro Pro Asp Ser Asn Ile Arg Leu Thr Thr Lys Ser 280 285 290 295	960
TTC CGA CCC TTC GTC CCA CGG TTA GCC AGG CTC TAC CCC AAC ATG AAC Phe Arg Pro Phe Val Pro Arg Leu Ala Arg Leu Tyr Pro Asn Met Asn 300 305 310	1008
CTG GAA CTC CAG GGA TCA GTG CCC TCT GCT CCG CTC CTG AAC TTC AGC Leu Glu Leu Gln Gly Ser Val Pro Ser Ala Pro Leu Leu Asn Phe Ser 315 320 325	1056
CCT GGG AAT CTG TCT GTG GAC CCC TAT ATG GAG ATA GAT GCC TTT GTG Pro Gly Asn Leu Ser Val Asp Pro Tyr Met Glu Ile Asp Ala Phe Val 330 335 340	1104
CTC CTG CCC AGC TCC AGC AAG GAG CCT GTC TTC CGG CTC AGT GTG GCC Leu Leu Pro Ser Ser Lys Glu Pro Val Phe Arg Leu Ser Val Ala 345 350 355	1152
ACT AAT GTG TCC GCC ACC TTG ACC TTC AAT ACC AGC AAG ATC ACT GGG Thr Asn Val Ser Ala Thr Leu Thr Phe Asn Thr Ser Lys Ile Thr Gly 360 365 370 375	1200
TTC CTG AAG CCA GGA AAG GTA AAA GTG GAA CTG AAA GAA TCC AAA GTT Phe Leu Lys Pro Gly Lys Val Lys Val Glu Leu Lys Glu Ser Lys Val 380 385 390	1248
GGA CTA TTC AAT GCA GAG CTG TTG GAA GCG CTC CTC AAC TAT TAC ATC Gly Leu Phe Asn Ala Glu Leu Leu Glu Ala Leu Leu Asn Tyr Tyr Ile 395 400 405	1296
CTT AAC ACC TTC TAC CCC AAG TTC AAT GAT AAG TTG GCC GAA GGC TTC Leu Asn Thr Phe Tyr Pro Lys Phe Asn Asp Lys Leu Ala Glu Gly Phe 410 415 420	1344
CCC CTT CCT CTG CTG AAG CGT GTT CAG CTC TAC GAC CTT GGG CTG CAG Pro Leu Pro Leu Leu Lys Arg Val Gln Leu Tyr Asp Leu Gly Leu Gln 425 430 435	1392
ATC CAT AAG GAC TTC CTG TTG GGT GCC AAT GTC CAA TAC ATG AGA Ile His Lys Asp Phe Leu Phe Leu Gly Ala Asn Val Gln Tyr Met Arg 440 445 450 455	1440
GTT Val	1443

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION: "rLBP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu Ala Leu Leu
-25 -20 -15 -10

Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly Leu Val Ala
-5 1 5

Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu Gly Leu Leu
10 15 20

Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp Phe Thr Gly
25 30 35

Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu Phe His Ser
40 45 50 55

Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu Arg Pro Val
60 65 70

Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser Ile Arg Val
75 80 85

Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu Gln Gly Ser
90 95 100

Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn Leu Leu Leu
105 110 115

Gly Ser Glu Ser Ser Gly Arg Pro Thr Val Thr Ala Ser Ser Cys Ser
 120 125 130 135

Ser Asp Ile Ala Asp Val Glu Val Asp Met Ser Gly Asp Leu Gly Trp
140 145 150

Leu Leu Asn Leu Phe His Asn Gln Ile Glu Ser Lys Phe Gln Lys Val
155 160 165

Leu Glu Ser Arg Ile Cys Glu Met Ile Gln Lys Ser Val Ser Ser Asp
170 175 180

Leu Gln Pro Tyr Leu Gln Thr Leu Pro Val Thr Thr Glu Ile Asp Ser
185 190 195

Phe Ala Asp Ile Asp Tyr Ser Leu Val Glu Ala Pro Arg Ala Thr Ala
200 205 210 215

Gln Met Leu Glu Val Met Phe Lys Gly Glu Ile Phe His Arg Asn His
220 225 230

Arg Ser Pro Val Thr Leu Leu Ala Ala Val Met Ser Leu Pro Glu Glu
235 240 245

His Asn Lys Met Val Tyr Phe Ala Ile Ser Asp Tyr Val Phe Asn Thr
250 255 260

Ala Ser Leu Val Tyr His Glu Glu Gly Tyr Leu Asn Phe Ser Ile Thr
265 270 275

Asp Glu Met Ile Pro Pro Asp Ser Asn Ile Arg Leu Thr Thr Lys Ser
 280 285 290 295
 Phe Arg Pro Phe Val Pro Arg Leu Ala Arg Leu Tyr Pro Asn Met Asn
 300 305 310
 Leu Glu Leu Gln Gly Ser Val Pro Ser Ala Pro Leu Leu Asn Phe Ser
 315 320 325
 Pro Gly Asn Leu Ser Val Asp Pro Tyr Met Glu Ile Asp Ala Phe Val
 330 335 340
 Leu Leu Pro Ser Ser Ser Lys Glu Pro Val Phe Arg Leu Ser Val Ala
 345 350 355
 Thr Asn Val Ser Ala Thr Leu Thr Phe Asn Thr Ser Lys Ile Thr Gly
 360 365 370 375
 Phe Leu Lys Pro Gly Lys Val Lys Val Glu Leu Lys Glu Ser Lys Val
 380 385 390
 Gly Leu Phe Asn Ala Glu Leu Leu Glu Ala Leu Leu Asn Tyr Tyr Ile
 395 400 405
 Leu Asn Thr Phe Tyr Pro Lys Phe Asn Asp Lys Leu Ala Glu Gly Phe
 410 415 420
 Pro Leu Pro Leu Leu Lys Arg Val Gln Leu Tyr Asp Leu Gly Leu Gln
 425 430 435
 Ile His Lys Asp Phe Leu Phe Leu Gly Ala Asn Val Gln Tyr Met Arg
 440 445 450 455
 Val

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..591

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (D) OTHER INFORMATION: "rLBP25"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCC AAC CCC GGC TTG GTC GCC AGG ATC ACC GAC AAG GGA CTG CAG TAT		48
Ala Asn Pro Gly Leu Val Ala Arg Ile Thr Asp Lys Gly Leu Gln Tyr		
1 5 10 15		
GCG GCC CAG GAG GGG CTA TTG GCT CTG CAG AGT GAG CTG CTC AGG ATC		96
Ala Ala Gln Glu Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile		
20 25 30		
ACG CTG CCT GAC TTC ACC GGG GAC TTG AGG ATC CCC CAC GTC GGC CGT		144
Thr Leu Pro Asp Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg		

35	40	45	
GGG CGC TAT GAG TTC CAC AGC CTG AAC ATC CAC AGC TGT GAG CTG CTT Gly Arg Tyr Glu Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu 50 55 60			192
CAC TCT GCG CTG AGG CCT GTC CCT GGC CAG GGC CTG AGT CTC AGC ATC His Ser Ala Leu Arg Pro Val Pro Gly Gln Gly Leu Ser Leu Ser Ile 65 70 75 80			240
TCC GAC TCC TCC ATC CGG GTC CAG GGC AGG TGG AAG GTG CGC AAG TCA Ser Asp Ser Ser Ile Arg Val Gln Gly Arg Trp Lys Val Arg Lys Ser 85 90 95			288
TTC TTC AAA CTA CAG GGC TCC TTT GAT GTC AGT GTC AAG GGC ATC AGC Phe Phe Lys Leu Gln Gly Ser Phe Asp Val Ser Val Lys Gly Ile Ser 100 105 110			336
ATT TCG GTC AAC CTC CTG TTG GGC AGC GAG TCC TCC GGG AGG CCC ACA Ile Ser Val Asn Leu Leu Gly Ser Glu Ser Ser Gly Arg Pro Thr 115 120 125			384
GTT ACT GCC TCC AGC TGC AGC AGT GAC ATC GCT GAC GTG GAG GTG GAC Val Thr Ala Ser Ser Cys Ser Ser Asp Ile Ala Asp Val Glu Val Asp 130 135 140			432
ATG TCG GGA GAC TTG GGG TGG CTG TTG AAC CTC TTC CAC AAC CAG ATT Met Ser Gly Asp Leu Gly Trp Leu Leu Asn Leu Phe His Asn Gln Ile 145 150 155 160			480
GAG TCC AAG TTC CAG AAA GTA CTG GAG AGC AGG ATT TGC GAA ATG ATC Glu Ser Lys Phe Gln Lys Val Leu Glu Ser Arg Ile Cys Glu Met Ile 165 170 175			528
CAG AAA TCG GTG TCC TCC GAT CTA CAG CCT TAT CTC CAA ACT CTG CCA Gln Lys Ser Val Ser Asp Leu Gln Pro Tyr Leu Gln Thr Leu Pro 180 185 190			576
GTT ACA ACA GAG ATT Val Thr Thr Glu Ile 195			591

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 197 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "rLBP25"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Asn Pro Gly Leu Val Ala Arg Ile Thr Asp Lys Gly Leu Gln Tyr
 1 5 10 15

Ala Ala Gln Glu Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile
 20 25 30

Thr Leu Pro Asp Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg

35

40

45

Gly Arg Tyr Glu Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu
50 55 60

His Ser Ala Leu Arg Pro Val Pro Gly Gln Gly Leu Ser Leu Ser Ile
65 70 75 80

Ser Asp Ser Ser Ile Arg Val Gln Gly Arg Trp Lys Val Arg Lys Ser
85 90 95

Phe Phe Lys Leu Gln Gly Ser Phe Asp Val Ser Val Lys Gly Ile Ser
100 105 110

Ile Ser Val Asn Leu Leu Leu Gly Ser Glu Ser Ser Gly Arg Pro Thr
115 120 125

Val Thr Ala Ser Ser Cys Ser Ser Asp Ile Ala Asp Val Glu Val Asp
130 135 140

Met Ser Gly Asp Leu Gly Trp Leu Leu Asn Leu Phe His Asn Gln Ile
145 150 155 160

Glu Ser Lys Phe Gln Lys Val Leu Glu Ser Arg Ile Cys Glu Met Ile
165 170 175

Gln Lys Ser Val Ser Ser Asp Leu Gln Pro Tyr Leu Gln Thr Leu Pro
180 185 190

Val Thr Thr Glu Ile
195